



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/511,345  
Source: PAT  
Date Processed by STIC: 10/27/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>) , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):  
U.S. Patent and Trademark Office, 220 20<sup>th</sup> Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 10/511,345

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      **Wrapped Nucleics**  
**Wrapped Aminos** The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2      **Invalid Line Length** The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3      **Misaligned Amino Numbering** The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4      **Non-ASCII** The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5      **Variable Length** Sequence(s)      contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6      **PatentIn 2.0 "bug"** A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s)     . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7      **Skipped Sequences (OLD RULES)** Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
 (2) INFORMATION FOR SEQ ID NO X (insert SEQ ID NO where "X" is shown)  
 (i) SEQUENCE CHARACTERISTICS (Do not insert any subheadings under this heading)  
 (xi) SEQUENCE DESCRIPTION SEQ ID NO X (insert SEQ ID NO where "X" is shown)  
 This sequence is intentionally skipped  
 Please also adjust the "(ii) NUMBER OF SEQUENCES" response to include the skipped sequences.
- 8      **Skipped Sequences (NEW RULES)** Sequence(s)      missing. If intentional, please insert the following lines for each skipped sequence:  
 <210> sequence id number  
 <400> sequence id number  
 000
- 9      **Use of n's or Xaa's (NEW RULES)** Use of n's and/or Xaa's have been detected in the Sequence Listing.  
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10      **Invalid <21> Response** Per 1.823 of Sequence Rules, the only valid <21> responses are Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <21> response is Unknown or is Artificial Sequence.
- 11      **Use of <220>** Use of <220> to <223> is MANDATORY if <21> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12      **PatentIn 2.0 "bug"** Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13      **Misuse of n/Xaa** "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid.



PCT

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/511,345

DATE: 10/27/2004  
TIME: 10:52:51

Input Set : A:\38331-0005.txt  
Output Set: N:\CRF4\10272004\J511345.raw

3 <110> APPLICANT: Kazuaki Hirasawa  
4 Akira Tsubokura  
5 Haruyoshi Mizuta  
8 <120> TITLE OF INVENTION: Method for Producing Canthaxanthin  
10 <130> FILE REFERENCE: 38331-0005  
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/511,345  
C--> 13 <141> CURRENT FILING DATE: 2004-10-15  
15 <150> PRIOR APPLICATION NUMBER: PCT/JP03/04398  
W--> 16 <151> PRIOR FILING DATE: 04-07-2003  
18 <150> PRIOR APPLICATION NUMBER: JP 2002-112240  
W--> 19 <151> PRIOR FILING DATE: 04-15-2002  
21 <160> NUMBER OF SEQ ID NOS: 2  
22 <170> SOFTWARE: PatentIn Ver. 2.0  
25 <210> SEQ ID NO: 1  
26 <211> LENGTH: 1452  
27 <212> TYPE: DNA  
28 <213> ORGANISM: Unknown  
30 <220> FEATURE:  
31 <223> OTHER INFORMATION: Description of Unknown Organism: E-396  
33 <400> SEQUENCE: 1  
34 agtttgatcc tggctcagaa cgaacgctgg cggcaggctt aacacatgca agtcgagcga 60  
35 gaccttcggg tctagcggcg gacgggtgag taacgcgtgg gaacgtgccc ttctctacgg 120  
36 aatagcccg ggaaactggg agtaataccg tatacgcct ttgggggaaa gatttatcgg 180  
37 agaaggatcg gccgcggtt gattaggtag ttggtgggt aatggccac caagccgacg 240  
38 atccatagct ggtttgagag gatgatcagc cacactggga ctgagacacg gccagactc 300  
39 ctacgggagg cagcagtggg gaatcttaga caatgggggc aacctgatc tagccatgcc 360  
40 gcgtgagtga tgaaggcctt agggttgtaa agctctttca gctgggaaga taatgacggt 420  
41 accagcagaa gaagcccg ctaactccgt gccagcagcc gcggaatac ggagggggct 480  
42 agcgttggtt ggaattactg ggcgtaaac gcacgtaggc ggactggaaa gtcagaggtg 540  
43 aaatcccagg gctcaacctt ggaactgcct ttgaaactat cagtctggag ttcgagagag 600  
44 gtgagtggaa ttccgagtgt agaggtgaaa ttcgtagata ttcggaggaa caccagtggc 660  
45 gaaggcggt cactggctcg atactgacgc tgaggtgcca aagcgtgggg agcaaacagg 720  
46 attagatacc ctggtagtcc acgcgtaaa cgatgaatgc cagacgtcgg caagcatgct 780  
47 tgcggtgtc acacctaacg gattaagcat tccgcctggg gactacggtc gcaagattaa 840  
48 aactcaaagg aattgacggg ggccgcaca agcgggtggg catgtggtt aattcgaagc 900  
49 aacgcgcaga accttaccac cccttgacat ggcaggaccg ctggagagat tcagctttct 960  
50 cgtaagagac ctgcacacag gtgctgcatg gctgtcgtca gctcgtgtcg tgagatgttc 1020  
51 ggtaagtcc ggcaacgagc gcaaccacg tccctagtgg ccagcaattc agttgggaac 1080  
52 tctatggaaa ctgccgatga taagtcggag gaaggtgtgg atgacgtcaa gtcctcatgg 1140  
53 gcttacggg ttgggtaca cactgtctac aatgggtggg acagtgggtt aatcccaaaa 1200  
54 agccatctca gttcggattg tctctgcaa ctcgaggga tgaagttgga atcgctagta 1260  
55 atcgcggaac agcatgccgc ggtgaatac ttcccgggc ttgtacacac cgcccgtcac 1320  
W--> 56 accatgggag ttggttctac ccgacgacn tgcgctaacc ttcggggggc aggcggccac 1380

Does Not Comply  
Corrected Diskette Needed

(PS.1-2)

PLS explain source of Genetic material

Invalid Response

pls see item #11 on error summary sheet.

pls see error explanation on page 4.

## RAW SEQUENCE LISTING

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Input Set : A:\38331-0005.txt

Output Set: N:\CRF4\10272004\J511345.raw

```

57 ggtaggatca gcgactgggg tgaagtcgta acaaggtagc cgtaggggaa cctgcggctg 1440
58 gatcacctcc tt 1452
60 <210> SEQ ID NO: 2
61 <211> LENGTH: 1426
62 <212> TYPE: DNA
63 <213> ORGANISM: Unknown
65 <220> FEATURE:
66 <223> OTHER INFORMATION: Description of Unknown Organism: A-581-1
68 <400> SEQUENCE: 2
69 tagagtttga tcttggtcga gaacgaacgc tggcggcagg cttaacacat gcaagtcgag 60
70 cgagaccttc gggctctagc gcgacgggt gagtaacgcg tgggaacgtg cccttctcta 120
71 cggaatagcc ccgggaaact gggagtaata ccgtatacgc cctttggggg aaagatttat 180
72 cggagaagga tggcccgcg ttggattagg tagttggtga ggtaacggct caccaagccg 240
73 acgatccata gctggtttga gaggatgac agccacactg ggactgagac acggcccaga 300
74 ctctacggg aggcagcagt ggggaatctt agacaatggg ggcaaccctg atctagccat 360
75 gccgcgtgag tgatgaaggc cttagggttg taaagctctt tcagctggga agataatgac 420
76 ggtaccagca gaagaagccc cggctaactc cgtgccagca gccgcggtaa tacggagggg 480
77 gctagcgttg ttcggaatta ctgggcgtaa agcgcacgta ggcggactgg aaagtcagag 540
78 gtgaaatccc agggctcaac cttggaactg cctttgaaac tatcagtctg gaggtcgaga 600
79 gaggtgagtg gaattccgag tgtagaggtg aaattcgtag atattcggag gaacaccagt 660
80 ggcgaaggcg gctcactggc tgcatactga cgctgaggtg cgaaagcgtg gggagcaaac 720
81 aggattagat accctggtag tccacgcgt aaacgatgaa tgccagacgt cggcaagcat 780
82 gcttgctcgt gtcacaccta acggattaag cattccgctt ggggagtagc gtcgcaagat 840
83 taaaactcaa aggaattgac gggggcccg cacaagcggg gagcatgtgg tttaattcga 900
84 agcaacgcgc agaaccctac caacccttga catggcagga ccgctggaga gattcagctt 960
85 tctcgtaaga gacctgcaca caggtgctgc atggctgtcg tcagctcgtg tcgtgagatg 1020
86 ttcggttaag tccggcaacg agcgcaacc acgtccctag ttgccagcat tcagttgggc 1080
87 actctatgga aactgccggt gataagccgg aggaaggtgt ggatgacgtc aagtcctcat 1140
88 ggcccttacg ggttgggcta cacacgtgct acaatggtgg tgacagtggg ttaatcccca 1200
89 aaagccatct cagttcggat tgcctctgc aactcgaggg catgaagttg gaatcgctag 1260
90 taatcgcgga acagcatgcc gcggtgaata cgttcccggg ccttgtagac accgcccgtc 1320
91 acaccatggg agttggttct acccgacgac gctgcgctaa cccttcgggg aggcaggcgg 1380
92 ccacggtagg atcagcgact ggggtgaagt cgtaacaagg tagcca 1426

```

pls explain source of genetic material.

Invalid Response

↑ pls see item #11  
on error summary sheet.

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/511,345

DATE: 10/27/2004  
TIME: 10:52:52

Input Set : A:\38331-0005.txt  
Output Set: N:\CRF4\10272004\J511345.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 1350

## VARIABLE LOCATION SUMMARY

PATENT APPLICATION: US/10/511,345

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TIME: 10:52:52

Input Set : A:\38331-0005.txt

Output Set: N:\CRF4\10272004\J511345.raw

Use of n's or Xaa's (NEW RULES): *Error Explanation: Ⓢ*  
Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
in <220> to <223> section, please explain location of n or Xaa, and which  
residue n or Xaa represents.

Seq#:1; N Pos. 1350

Best Available Copy

## VERIFICATION SUMMARY

PATENT APPLICATION: US/10/511,345

DATE: 10/27/2004

TIME: 10:52:52

Input Set : A:\38331-0005.txt

Output Set: N:\CRF4\10272004\J511345.raw

L:12 M:270 C: Current Application Number differs, Replaced Application Number  
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:16 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD  
L:19 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD  
L:56 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:1  
L:56 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:1  
L:56 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:1320

**Best Available Copy**